

Amendments to the Claims:

1-57. (canceled)

58. (currently amended) An isolated polypeptide having at least 80% amino acid sequence identity to:

(a) the amino acid sequence of the polypeptide of SEQ ID NO:330 shown in Figure 132 (SEQ ID NO:330);

(b) the amino acid sequence of the polypeptide of SEQ ID NO:330 shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide;

(c) ~~the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 132 (SEQ ID NO:330);~~

(d) ~~the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide; or~~

[[e)] (c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209772,

wherein the polypeptide inhibits the uptake of glucose or FFA (free fatty acid) by adipocyte cells.

59. (currently amended) The isolated polypeptide of Claim 58 having at least 85% amino acid sequence identity to:

(a) the amino acid sequence of the polypeptide of SEQ ID NO:330 shown in Figure 132 (SEQ ID NO:330);

(b) the amino acid sequence of the polypeptide of SEQ ID NO:330 shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide;

~~(e) — the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 132 (SEQ ID NO:330);~~

~~(d) — the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide; or~~

[[~~(e)~~]] (c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209772,

wherein the polypeptide inhibits the uptake of glucose or FFA (free fatty acid) by adipocyte cells.

60. (currently amended) The isolated polypeptide of Claim 58 having at least 90% amino acid sequence identity to:

(a) the amino acid sequence of the polypeptide of SEQ ID NO:330 ~~shown in Figure 132 (SEQ ID NO:330);~~

(b) the amino acid sequence of the polypeptide of SEQ ID NO:330 ~~shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide;~~

~~(e) — the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 132 (SEQ ID NO:330);~~

~~(d) — the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide; or~~

[[~~(e)~~]] (c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209772,

wherein the polypeptide inhibits the uptake of glucose or FFA (free fatty acid) by adipocyte cells.

61. (currently amended) The isolated polypeptide of Claim 58 having at least 95% amino acid sequence identity to:

(a) the amino acid sequence of the polypeptide of SEQ ID NO:330 shown in Figure 132 (SEQ ID NO:330);

(b) the amino acid sequence of the polypeptide of SEQ ID NO:330 shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide;

(e) ~~the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 132 (SEQ ID NO:330);~~

(d) ~~the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide; or~~

[[~~(e)~~]] (c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209772,

wherein the polypeptide inhibits the uptake of glucose or FFA (free fatty acid) by adipocyte cells.

62. (currently amended) The isolated polypeptide of Claim 58 having at least 99% amino acid sequence identity to:

(a) the amino acid sequence of the polypeptide of SEQ ID NO:330 shown in Figure 132 (SEQ ID NO:330);

(b) the amino acid sequence of the polypeptide of SEQ ID NO:330 shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide;

(e) ~~the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 132 (SEQ ID NO:330);~~

(d) ~~the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide; or~~

[[~~(e)~~]] (c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209772,

wherein the polypeptide inhibits the uptake of glucose or FFA (free fatty acid) by adipocyte cells.

63. (currently amended) An isolated polypeptide comprising:

(a) the amino acid sequence of the polypeptide of SEQ ID NO:330 shown in Figure 132 (SEQ ID NO:330);

(b) the amino acid sequence of the polypeptide of SEQ ID NO:330 shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide;

~~(c) the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 132 (SEQ ID NO:330);~~

~~(d) the amino acid sequence of the extracellular domain of the polypeptide shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide; or~~

[[~~(e)~~]] (c) the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209772.

64. (currently amended) The isolated polypeptide of Claim 63 comprising the amino acid sequence of the polypeptide of SEQ ID NO:330 shown in Figure 132 (SEQ ID NO:330).

65. (currently amended) The isolated polypeptide of Claim 63 comprising the amino acid sequence of the polypeptide of SEQ ID NO:330 shown in Figure 132 (SEQ ID NO:330), lacking its associated signal peptide.

66. (canceled)

67. (canceled)

68. (previously presented) The isolated polypeptide of Claim 63 comprising the amino acid sequence of the polypeptide encoded by the full-length coding sequence of the cDNA deposited under ATCC accession number 209772.

69. (previously presented) A chimeric polypeptide comprising a polypeptide according to Claim 58 fused to a heterologous polypeptide.

70. (previously presented) The chimeric polypeptide of Claim 69, wherein said heterologous polypeptide is an epitope tag or an Fc region of an immunoglobulin.